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M S D V T I V K E G W V Q K R G E 17
 1 GGGAGTCATCATGAGCGATGTTACCATTGTGAAAGAAGGTTGGGTTTCAGAAGAGGGGAGA
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 Y K E K P Q D V D L P Y P L N N F S V A 57
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 K C O L M K T E R P K P N T F I I R C L 77
 181 AAAATGCCAGTTAATGAAAACAGAACGACCAAAGCCAAACACATTTATAATCAGATGTCT
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 241 CCAGTGGACTACTGTTATAGAGAGAACATTTTCATGTAGATACTCCAGAGGAAAGGGAAGA
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 421 AACCCATCATAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGTAAAGG
 T F G K V I L V R E K A S G K Y Y A M K 177
 481 CACTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAAATACTATGCTATGAA
 I L K K E V I I A K D E V A H T L T E S 197
 541 GATTCTGAAGAAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAAAG
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 601 CAGAGTATTAAAGAACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTCCAGAC
 K D R L C F V M E Y V N G G E L F F H L 237
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 D C M D N E R R P H F P O F S Y S A S G 477
 1381 GGACTGCATGGACAATGAGAGGCGGCCGATTTCCCTCAATTTTCTACTCTGCAAGTGG
 R E 479
 1441 ACGAGAATAAGTCTCTTTCATTCTGCTACTTCACTGTCTCTTCAATTTATTACTGAAAA
 1501 TGATTCTGACATCACCAGTCTTAGCTCTTACACATAGCAGGGGCA

Figure 1

Figure 2

Akt-1	: MSDVAIVKESGHLHKGGEYIKNTMRPRYFLKNDGTFIGYKERFQDVLCREAEINNFPSVACQQLMKTEREPNTFIIRCLQMTTVIERPHW	: 90
Akt-2	: MNEVSVIKESGHLHKGGEYIKNTMRPRYFLKNDGTFIGYKERFQDVLCREAEINNFPSVACQQLMKTEREPNTFIIRCLQMTTVIERPHW	: 90
Akt-3	: MSDVTVIKESGHLHKGGEYIKNTMRPRYFLKNDGTFIGYKERFQDVLCREAEINNFPSVACQQLMKTEREPNTFIIRCLQMTTVIERPHW	: 89
Akt-1	: ETEPEREEMTTSITQTVADGLKKQE--EEEMDFRSQSPSDNSGAEEMEVSILAKPKHRTVTMMNEFEYLKLLGKGTGFGKVLVKKERATGRYYAM	: 178
Akt-2	: DSEDEREEMPRALICMWANSILKORAPGEDDNDYKCGSPSDSSSTTEEMEVAVSARAKAVTMMNDFYLLKLLGKGTGFGKVLVKKERATGRYYAM	: 180
Akt-3	: DTEPEREEMTTSITQTVADGLKKQE--EERQNCSPSTQILDNIQEEEDDASTTHHK-RKTMNDFDYLLKLLGKGTGFGKVLVKKERATGRYYAM	: 176
Akt-1	: KILNKEVTVAKDEVAHTLTENRVLQMSRHPELTALKYSPQTHDRLCFVMEYANGGELFFPHLSPERVFPSEDPARFYGAETVSALDYLHSEK	: 268
Akt-2	: KILRKEVTVAKDEVAHTLTESRVLQMSRHPELTALKYAFQTHDRLCFVMEYANGGELFFPHLSRERVPTEERARFYGAETVSALDYLHSE-R	: 269
Akt-3	: KILRKEVTVAKDEVAHTLTESRVLQMSRHPELTALKYSPQTKORLCFVMEYVMSSELFFPHLSRERVPSEDPTRFYGAETVSALDYLHSE-G	: 265
Akt-1	: NVVYRDILKLENMLDKDGHKIKITDPGLCKNEGTIKIGATMKTFQGTPEXYLAPEVLEDNDYGRAVLMMGLGVVMYEMMCGRLPFFYNQDHEKLF	: 358
Akt-2	: DVVYRDILKLENMLDKDGHKIKITDPGLCKNEGTISDGATMKTFQGTPEXYLAPEVLEDNDYGRAVLMMGLGVVMYEMMCGRLPFFYNQDHEKLF	: 359
Akt-3	: KIVYRLLKLENMLDKDGHKIKITDPGLCKNEGTILATMKTFQGTPEXYLAPEVLEDNDYGRAVLMMGLGVVMYEMMCGRLPFFYNQDHEKLF	: 355
Akt-1	: ELILMEEIRFPFTLSPEAKSLLSELLKKNDKORLGGSESDANEIMCHRPACHIVMCHVIERKLSPPFPQVTSSETDTRYFDDEEFTACMLT	: 448
Akt-2	: ELILMEEIRFPFTLSPEAKSLLAELLKNDKORLGGSESDANEVMEHRPFLSINMQDMVQKHLPEEPKQVTSSEVDTRYFDDEFTACSLT	: 449
Akt-3	: ELILMEDIRFPFTLSPEAKSLLSELLKNDKORLGGSESDANEIMRSEFSEVNMQDMVDKHLVPEEPKQVTSSETDTRYFDDEEFTACMLT	: 445
Akt-1	: ITPEDQDQS--MEQVLSERRPHFPQPSYSASGTA	: 480
Akt-2	: ITPEDRYDS--IGLELDDQTHFPQPSYSASIRE	: 481
Akt-3	: ITPEEKIDEDGDQMDQNERPHFPQPSYSASGRE	: 479

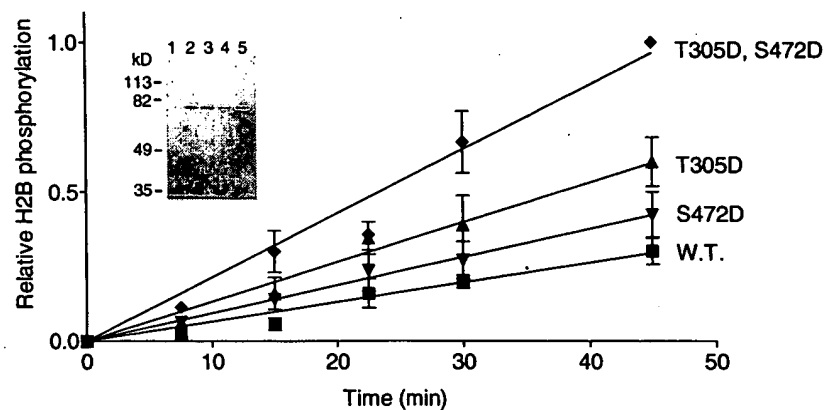
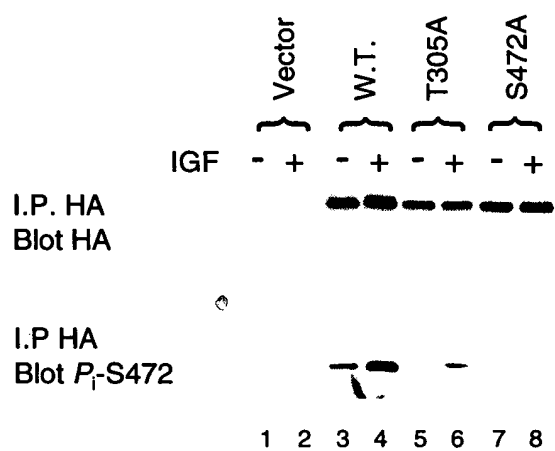
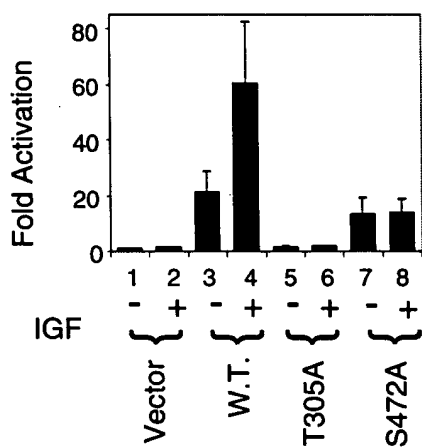
A**B****C**

Figure 3

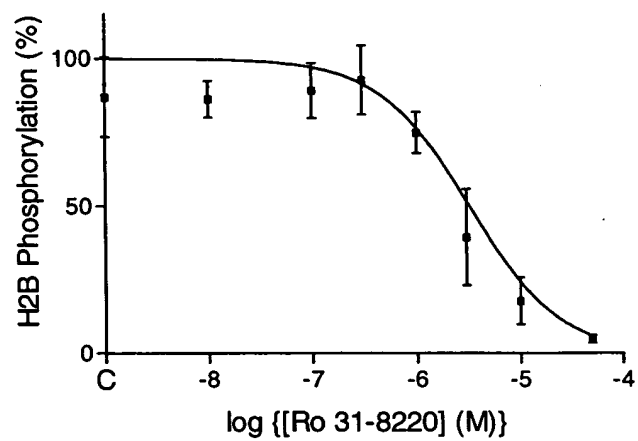
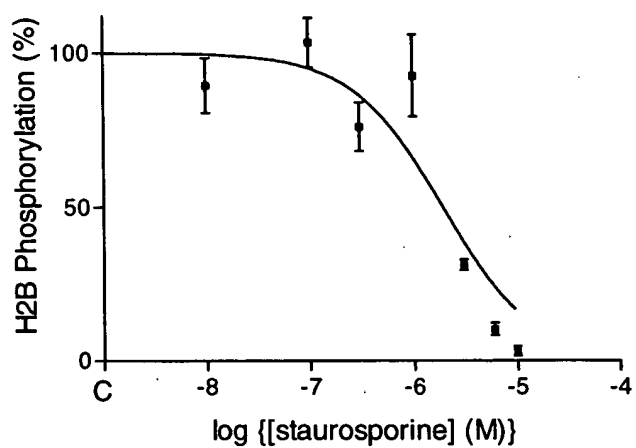


Figure 4.

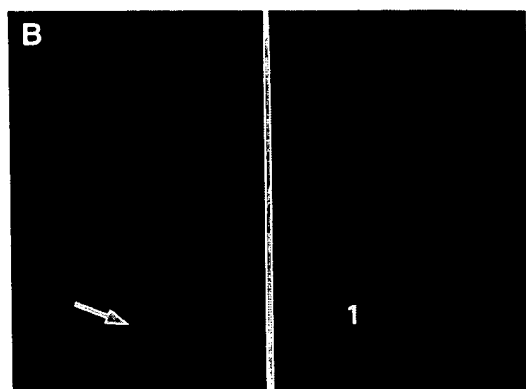
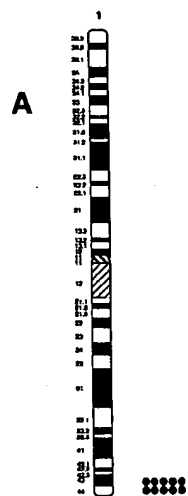


Figure 5

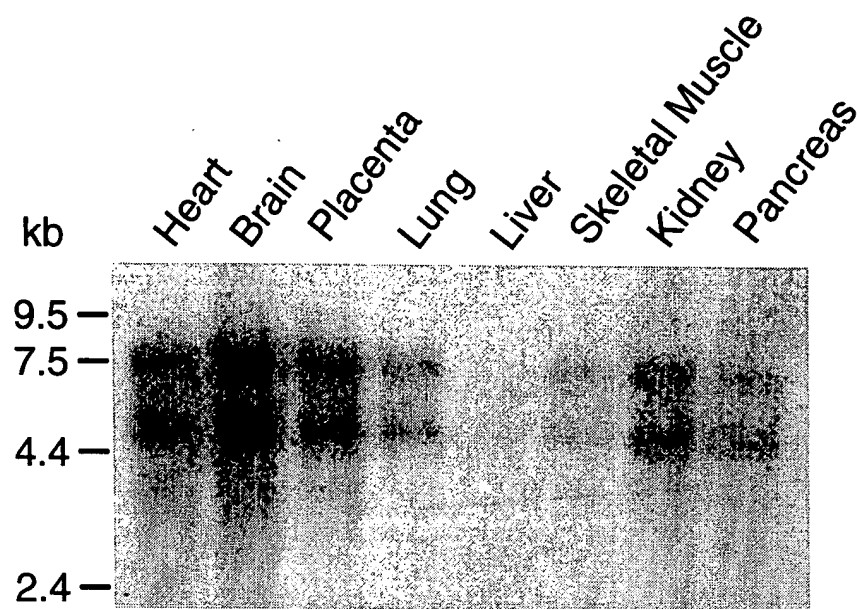


Figure 6A

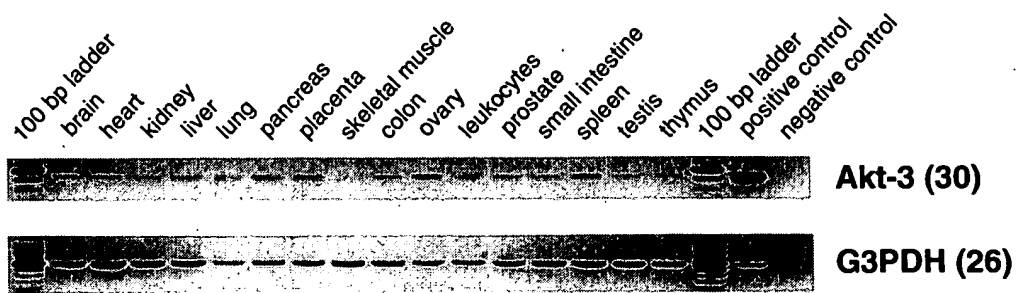


Figure 6B

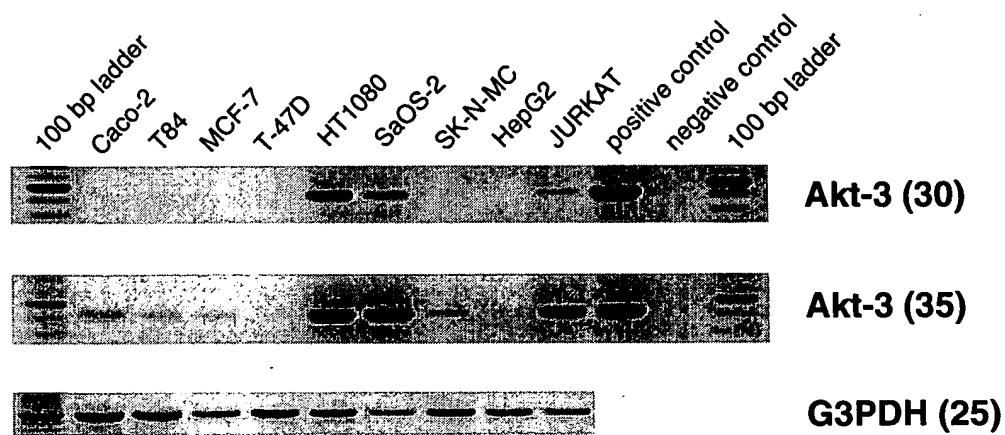


Figure 6C

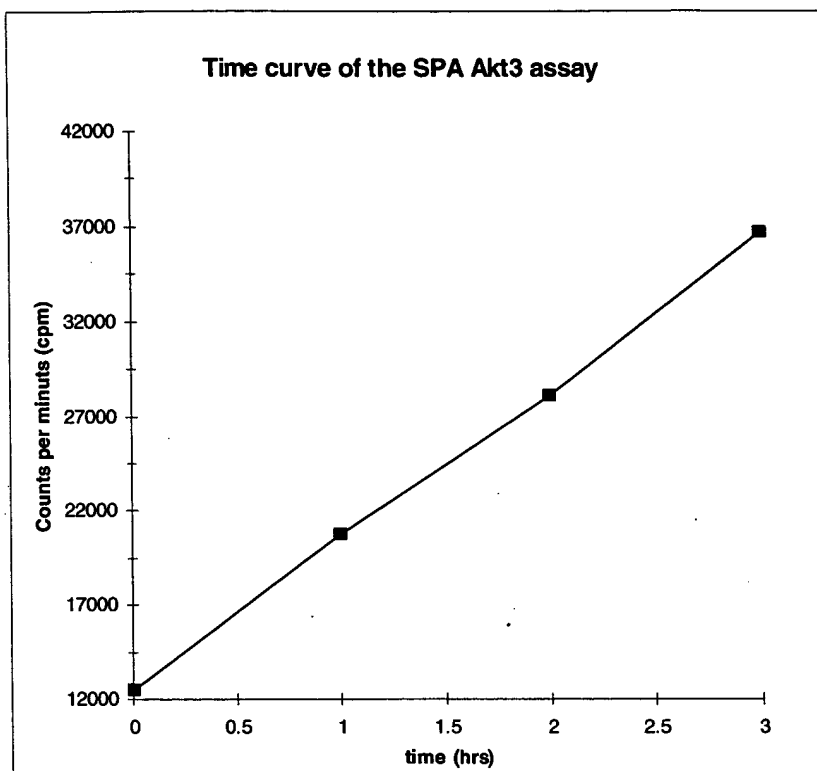


Figure 7

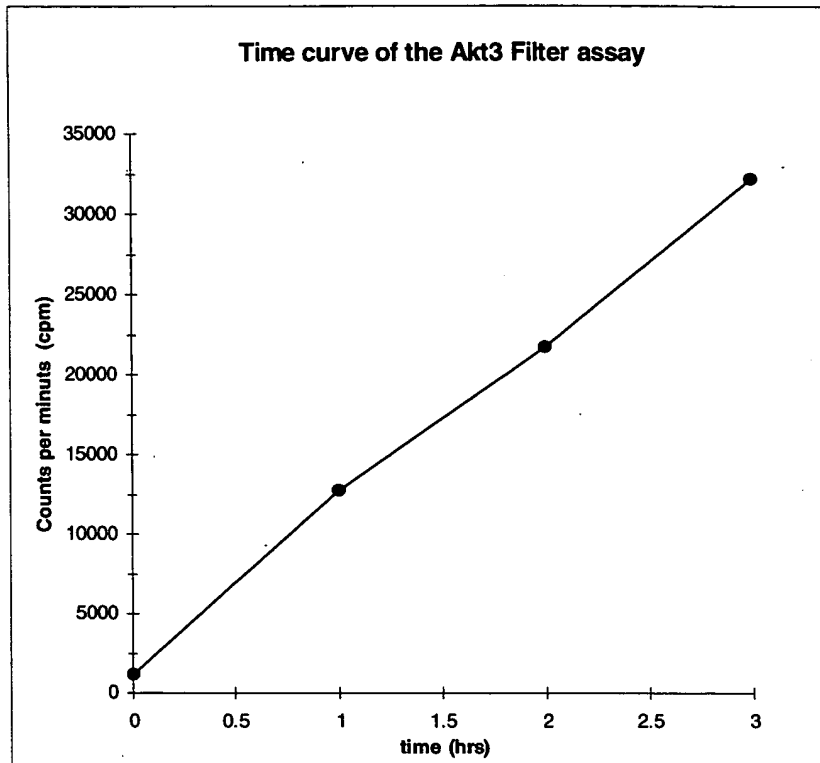


Figure 8

FIG. 2

Akt-1	MSDVAVKEGWLHKGGEYKWTWRPRYELLKNDGTFIGYKERPDVDQREAPLNINFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHV	: 90
Akt-2	MNEVSVJKEGWLHKGGEYKWTWRPRYELLKSDGSFIGYKERPEAPDQTLPLNINFSVAECQLMKTERPRPNTFIIRCLQWTTVIERTFHV	: 90
Akt-3	MSDVTIKEGWVQKRGEYKINWRPRYELLKTDGSFIGYKEKPODVDLP-YPLNINFSVAKCOLMKTERPKPNTFIIRCLQWTTVIERTFHV	: 89
Akt-1	ETPEEREETITAIQITVADGLKKQE--EEEMDFRSGSPSDNSGAEEEMVSLAKPKHRTVMNTEPEYLLKLGKGTGKGVILVKEKATGRYYAM	: 178
Akt-2	DSPDEREEWMRAIQMWANSIKQAPGEDPMDYKCGSPSDSSITTEEMEVAVSKARAKVTMNDPDYLLKLGKGTGKGVILVREKATGRYYAM	: 180
Akt-3	DTPEEREETITAIQAVADRILQRE--EERVNCSPTSQIDNIGEEEMDASTTHKPKTKMNDPDYLLKLGKGTGKGVILVREKASGKYYAM	: 176
Akt-1	KILKKEVIAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDPRARFYGAIEVSALDYLHSEK	: 268
Akt-2	KILKEVIAKDEVAHTLTESRVLQNTRHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVFEERARFYGAIEVSALDYLHS-R	: 269
Akt-3	KILKKEVIAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTKDRLCFVMEYANGGELFFHLSRERVFSEDRTIRFYGAIEVSALDYLHS-G	: 265
Akt-1	NVYRDLKLENMLDKDGHKITDFGLCKEGIKDGATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNQDHEKLF	: 358
Akt-2	DVYRDLKLENMLDKDGHKITDFGLCKEGISDGGATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNQDHERLF	: 359
Akt-3	KIVYRDLKLENMLDKDGHKITDFGLCKEGITDAATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNQDHEKLF	: 355
Akt-1	ELILMEEIRFPRTLGPPEAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRRFFAGVWQHIVYEKKLSPPEKPOVTSETDTRYFDEEFTAQMIT	: 448
Akt-2	ELILMEEIRFPRTLGPPEAKSLLAGLLKKDPKQRLGGGSDAKEVMEHRRFLSINWQDVWQKKLLPPPEKPOVTSEVDTRYFDDDEFTAQSIIT	: 449
Akt-3	ELILMEDIKFPRTLSSDAKSLLSGLLJKDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPPEKPOVTSETDTRYFDEEFTAQITIT	: 445
Akt-1	ITPPDQDDDS--MEGVDSERRPHFPQFSYASGTA	: 480
Akt-2	ITPPDRYDS--LGLLELDQRTHFQFSYASIRE	: 481
Akt-3	ITPPEKYDEDGMDQMDNERRPHFPQFSYASGRE	: 479

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